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RNA-Seq Analysis and *de novo* Transcriptome Assembly of *Coffea arabica* and *Coffea eugenioides*

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Coffee is one of the most important agricultural commodites in the world. *Coffea arabica*, an allotetraploid from a recent hybridization of two diploid species (*C.canephora* and *C.eugenioides*) is responsible for 70% of world commercial production. Recent studies have been done to analyse transcriptome data of *Coffea* spp. in order to improve our knowledge in genetics and gene expression of those species. However, there is few data on coffee fruit transcriptome. In this work, RNA-Seq of two organs (whole fruit – cherry stage and mature leaves) from allotetraploid *C. arabica* cv. Mundo Novo and its diploid ancestor *C.eugenioides*, were done using Illumina HiSeq 2000 (100 bp single-end sequences). We report the generation of near 10 million reads for *C.arabica* (4,747,049 of fruits and 6,156,750 reads of leaves) and 7,5 million reads for *C.eugenioides* (3,688,364 of fruits and 3,835,373 reads of leaves). *De novo* assembly and digital gene expression analyses was performed to generate a collection of 35,462 contigs from *C.arabica* cv. Mundo Novo (average length of 691 bp) and 36,935 contigs of *C.eugenioides* (average length of 701 bp). Funnctional annotation were performed by sequence comparison with public databases (NCBI-nr, Swiss-prot and PlantCyc). Our results showed the presence of prevalent genes and species-specific either in *C.arabica* or *C.eugenioides* that could explain particular characteristics of these two species. Characterization of *Coffea spp*. transcriptome provides an effective tool for better understanding for differential gene expression in *Coffea* spp., providing important clues of *C.arabica* gene evolution, as well as valuable information for coffee breeding.